

GenCore version 5.1.7
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OM protein - protein search, using bw model

Run on: April 14, 2006, 01:34:23 ; Search time 75 Seconds

(without alignments)
3648.671 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000

Perfect score: 15748

Sequence: 1 MAEAGGASBQDDVSPFLRTB.....RLADNADHWAKKKKEELVT 3000

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12295	78.1	5126	2	540450
2	6828	43.0	5107	2	729144
3	6770.5	43.0	4969	2	A57113
4	6769	43.0	4967	2	872269
5	6534.5	41.5	5037	1	A54161
6	6453.5	41.0	5035	1	146646
7	6442.5	40.9	5032	1	A35041
8	6439	40.9	5037	2	B35041
9	6438.5	40.9	4859	2	874173
10	6423	40.8	4869	2	866572
11	6419	40.8	4868	2	B54161
12	6413	40.7	4872	2	827272
13	538	3.4	163	2	147214
14	520	3.3	162	2	147213
15	327	2.1	2783	2	T31431
16	323	2.1	2701	2	817796
17	296.5	1.9	2693	2	A40743
18	292.5	1.9	2695	2	854974
19	290.5	1.8	2670	2	A46719
20	289	1.8	2713	2	A55713
21	286.5	1.8	2734	2	B36579
22	285	1.8	2671	2	A49873
23	284	1.8	1966	2	T32552
24	284	1.8	2848	2	T32550
25	279	1.8	2749	1	ACM57T
26	279	1.8	2749	2	A36579
27	277.5	1.8	2833	2	A43360
28	205	1.3	1676	2	B71410
29	203.5	1.3	2541	2	T29340

30	198	1.3	3259	1	A56539	giantin - human
31	198	1.3	5369	2	T44807	myosubtilin synth
32	197.5	1.3	2954	2	T14156	kinesin-related pr
33	196.5	1.2	2218	2	B84683	hypothetical prote
34	192	1.2	1727	2	T50073	myosin-like coiled
35	192	1.2	3225	2	I52300	giantin - human
36	191	1.2	1882	2	T00069	hypothetical prote
37	189.5	1.2	2663	1	S28261	centromere protein
38	188.5	1.2	1642	2	T08880	NMDA receptor-bind
39	188	1.2	4540	2	T30838	cytoplasmic dynein
40	182.5	1.2	2331	2	T25410	hypothetical prote
41	182.5	1.2	3187	2	JC5837	36k Golgi complex
42	180.5	1.1	2712	2	T05113	hypothetical prote
43	179	1.1	6669	2	S55024	nebulin, skeletal
44	178	1.1	4151	2	T13734	groovin gene prote
45	177	1.1	52	2	I46644	ryanodine receptor

ALIGNMENTS

RESULT 1
S40450
ryanodine receptor/calcium release channel - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
C:Accession: S40450

R:Takehima, H.; Nishi, M.; Iwabe, N.; Miyata, T.; Hosoya, T.; Masai, I.; Hotta, Y.
FEBS Lett. 337, 81-87, 1994

A:Title: Isolation and characterization of a gene for a ryanodine receptor/calcium rel
A:Reference number: S40450; MUID:94102409; PMID:8276118

A:Accession: S40450

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5126 <TRX>

A:Cross-references: UNIPARC:UP1000017CF36

C:Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 home

Query Match 78.1%; Score 12295; DB 2; Length 5126;
Best Local Similarity 77.5%; Pred. No. 0;
Matches 2348; Conservative 275; Mismatches 338; Indels 68; Gaps 22;

Qy	1	MAEAGGASBQDDVSPFLRTBDMVCLCTATGGRVCLAEFGNHCLENADKNPPDL 60	
Db	1	MAEAGG-SBQDDVSPFLRTBDMVCLCTATGGRVCLAEFGNHCLENADKNPPDL 59	
Qy	61	SOCPFYVBOALSVBALQELVTAAGSEFGKGTGSHRTLYGNALILRHNSDMYLAIST 120	
Db	60	SOCPFYVBOALSVBALQELVTAAGSEFGKGTGSHRTLYGNALILRHNSDMYLAIST 119	
Qy	121	SSSQDKLAPVGLQOHSQGEACMWTLPASKORSSEKVRVGDLLIVSVATERYLAATTK 180	
Db	120	SSSQDKLSFDVGLQHSQGEACMWTLPASKORSSEKVRVGDLLIVSVATERYLAATTK 179	
Qy	181	ENEVSYVNASFHVTHMSVOPYGTGISPMKYGVYFGVDVLRFPFGDDECLTIPSTWKDG 240	
Db	180	ENEGSYVNASFHVTHMSVOPYGTGISPMKYGVYFGVDVLRFPFGDDECLTIPSTWKDEA 239	
Qy	241	GQNTVVTGGSVWSQASNLRLRLARPKAGGFLNTHPMKIRITTTGRTLYGVNDQNELY 300	
Db	240	GQNTVVTGGSVWSQASNLRLRLARPKAGGFLNTHPMKIRITTTGRTLYGVNDQNELY 299	
Qy	301	LVSEERATTSACAFLEQEKDDQVLEKQVLEKQVLEKQVLEKQVLEKQVLEKQVLEKQV 360	
Db	300	LVKSEASLATTTSW-QEKDEKQVLEKQVLEKQVLEKQVLEKQVLEKQVLEKQVLEKQV 358	
Qy	361	KSYETKKKGKGVKVEKQALIHBEKMDGLDPSRQSEESRTAIVKCSLFTKPNGL 420	
Db	359	KSYETKKKGKGVKVEKQALIHBEKMDGLDPSRQSEESRTAIVKCSLFTKPNGL 418	
Qy	421	ETLQENRRHGMFPASVNLGEMVWKLDELINYPAPDDMEHEKONFRALRNODLFOE 480	
Db	419	ETLQENRRHGMFPASVNLGEMVWKLDELINYPAPDDMEHEKONFRALRNODLFOE 478	

[illegible]

QY	1552	GVR.IY.PQGD.PHHY.IGWTTQYHLSGD.PNOS.KYTKS.VII.ITDDY.DRV.VENW.NOS.CMV	161.1
Db	1534	GVR.IY.PQGD.PHHY.IGWTTQYHLSHSEBFNNKRRGS.VI.IEDDY.EA.IE.IE.IDOS.CTV	159.3
QY	1612	RADLE.YNE.VWA.EA.ANKA.GSQM.PIG.CSV.DI.STGS.VS.FTC.BE.KD.TS.FFK.KME.PE.KL.PPA.I	167.1
Db	1594	RADLE.FRE.VN.QDAS.GKAS.QGM.FV.GCY.DTAT.GI.I.RFT.CS.KD.I.SHHMMH.PD.KL.PPA.I	165.3
QY	1672	FVEATSK.EI.IQ.IE.I.GRSAT.SI.PLSA.VL.PTSDKE.VI.IQ.PPRL.KVOC.I.KPH.QA.RVP.NOS	173.1
Db	1654	FVEATSK.EI.IQ.IE.I.GRSAT.PTTL.PLSA.VL.PTSDK.I.NFOS.PRL.KVOC.I.RPH.QA.RVP.NTA	173.3
QY	1732	LOYVAL.KLSD.RGSMT.CE.DAVSML.AH.IBE.BE.CD.IILB.IEMD.KLS.PHSHTL.T.YAA	179.1
Db	1714	LOYVAL.KLSD.RGSMT.CE.DV.SML.AH.IBE.BE.CD.ILE.IEMD.KLS.PH.ASHL.T.YAA	177.3
QY	1792	LCYOSN.RA.AHAL.CTH.DOK.IYAL.IOSQVW.SG.RGQFYD.I.LTAL.HLSHA.TMBA.CKN	185.1
Db	1774	LCYOSN.RA.AHAL.CQH.DQK.IYAL.ISTBYMSG.LRGQFD.I.LTAL.HLSHA.TMBA.CKN	183.3
QY	1852	EF.VI.PL.GPEL.KAL.YEB.DMGHS.IRS.IQ.TES.VR.PQM.KTD.I.-----ABSITE	189.7
Db	1834	EY.IY.PL.GA.MEL.KEL.YS.DBEM.GHS.I.RSLV.TES.VR.PQL.RMT.BIT.PY.IAT.SMP.SV.SB.PID	189.3
QY	1898	IS.NI.YSY.PY.PLE.VAR.EV.MQAL.AE.VTQV.NHR.DP.VGGS.NE.NI.PL.I.KL.VD.LL.VGM	195.7
Db	1894	IDQ.IY.SR.PF.PLE.VR.QO.MEAL.KDA.VI.NO.VH.ND.P.IGM.NE.NI.PL.I.KL.TD.LL.VGV	195.3
QY	1958	MR.DE.VK.LL.I.MT.PE.TM.DS.PD.EG.ED.EHR.KGL.I.HMKM.AGAL.QM.CYLL.OH.ND.O.LR	201.7
Db	1954	LTD.DVOR.LM.I.D.PE.TM.DQ.FE.BE.GD.EHR.KGL.I.HMKM.AGAL.QM.CYLL.HH.I.YDQ.LR	201.3
QY	2018	HR.VE.A.I.IA.FAH.DF.VGD.IQ.TQ.LR.YTE.I.KOSD.P.SA.VAA.KT.RB.FR.CP.PRE.ONNA.I.SFK	207.7
Db	2014	HR.VE.S.IA.FSH.DF.VGD.IQ.TQ.LR.YTE.I.KOSD.P.SA.VAA.KT.RB.FR.CP.PRE.ONNA.I.CFK	207.3
QY	2078	HLE.BE.DK.E.NC.PC.SEEL.I.A.R.NM.FH.DT.MA.VS.LHAL.OEP.DA.E.NO.S-PEAK.PGA.FGL.I.N	213.6
Db	2074	NLE.BPD.DN.CT.CG.IE.LR.GAD.PF.DS.I.MOKV.SI.MAL.OB.PGV.ECTA.I.EVYTG.P.I.TY.I.N	213.3
QY	2137	I.I.N.VV.KEL.EE.BA.KA.I.BE.PPKT.PE.KR.KYL.I.O.IY.VMA.E.SQ.I.E.TKL.VR.E.MS.L.VRO	219.6
Db	2134	P.I.N.VV.KEL.EE.PK.EVE.BE.PKCT.PE.VR.KYL.I.K.IY.VMA.E.SQ.I.E.NP.L.VR.E.MS.S.L.RQ	219.3
QY	2197	YD.AV.GE.I.RA.L.EK.TY.V.NA.KT.KL.DV.AE.MV.GL.SQ.I.RA.LL.EV.O.NS.QE.EE.I.M.R.KL.MC.VN	225.6
Db	2194	YD.YT.GE.L.VR.A.L.EK.TY.V.NT.A.RD.VA.E.MV.GL.SQ.I.RA.LL.EV.O.NS.QE.EE.I.M.R.KL.MC.VN	225.3
QY	2257	NHTE.FQ.HD.I.I.R.VL.R.VHE.NV.WA.VM.MNT.LG.RA.O.QSDA.O.SS.O.PVAE--DSKEKOTSHEM	231.4
Db	2254	NAT.FQ.HD.I.I.R.I.L.R.VHE.NV.WA.VM.MNT.I.GRA.O.QSDA--PTOSEVA.GAPS.KEDOTSHEM	231.2
QY	2315	VVA.ACCR.LC.FC.RTRGR.NO.CAM.DHP.LL.E.NS.II.LS.RS.LG.S.TP.LD.VA.YSS.I.M.NTE	237.4
Db	2313	VVA.ACCR.LC.FC.RTRGR.NO.CAM.DHP.LL.D.NN.A.II.LAR.SL.RKSTP.LD.VA.YSS.I.M.NTE	237.2
QY	2375	I.A.LA.LR.EHY.L.EK.IA.VY.SR.CG.LOS.NS.E.LY.EK.GY.PD.LC.MD.PV.EGER.YU.D.P.L.F.CV.WA.GAS	243.4
Db	2373	I.A.LA.LR.EHY.L.EK.IA.VY.SR.CG.LOS.NS.E.LY.EK.GY.PD.LC.MD.PV.EGER.YU.D.P.L.F.CV.WA.GAS	243.2
QY	2435	VBEN.NA.VI.R.LL.I.R.PE.CT.G.PAL.R.GE.BG.LL.KA.I.VDANKV.S.E.R.IA.RR.KL.E.ME.QE.GD.V-	249.3
Db	2433	VBEN.NA.VI.R.LL.I.R.PE.CT.G.PAL.R.GE.BG.G.F.PA.I.VE.NR.MS.E.R.I.SD.CK.MQD--BAEGTIA	249.1
QY	2494	--NPS.HL.PE.SD.DEDY.I.DTGA.I.I.NFY.CT.VL.DL.GC.AD.AS.TY.EG.KN.E.SI.RA.RA.SLR	255.1
Db	2492	GLNFT.HE.L.PGE.BE.DEDY.I.DTGA.I.I.NFY.CT.VL.DL.GC.AD.AS.TY.EG.KN.E.SI.RA.RA.SLR	255.1
QY	2552	SL.VL.EJL.OGV.LA.SR.FL.NN.PA.AGE.BE.PK.SD.MP.SGL.PG.KOSV.GL.PL.EV.VY.GI.E.TO.E.LF	261.1
Db	2552	SL.VL.EJL.OGV.LA.SR.FL.NN.PA.AGE.BE.PK.SD.MP.SGL.PG.KOSV.LF.L.EV.VY.GI.EA.DL.F	261.1
QY	2612	YK.LLE.BA.FE.DL.DR.AAT.ML.DR.ND.CE.SD.MAL.SM.NR.Y.I.GNS.I.LL.P.LI.I.KHAY.YN.EA.NY.ASL	267.1

Db 2612 YRLBDAFPLDTATATILKSDGSDMDALANRYIGNSILPLLKSKSKFYNEAENYASL 2671
Qy 2672 LQATHTVRLSKNRLTKGOREAVSDPLVALTSAQPSMLTLRLTYDVSKSEYTT 2731
Db 2672 LQATHTVRLSKNRLTKGOREAVSDPLVALTSAQPSMLTLRLTYDVSKSEYTT 2731
Qy 2732 VALRLTLHYERCAKYGTGACQAFGASDDEKELTWMLPSNIPDSKMDYBELPQ 2791
Db 2732 VALRLTLHYERCAKYGTGACQAFGASDDEKELTWMLPSNIPDSKMDYBELPQ 2791
Qy 2791 KALPCLIAIGCALPPYSLSKNTDBDYGRKMGAP--DQPYMNPIDITNVHLDNDLNS 2848
Db 2851 IYQKSEHVDAMASRKIRNGWYGGWSQKTHPLRKYNNMLNDYKERYKPEVRESI 2911
Qy 2849 LVQKSEHVDAMASRKIRNGWYGGWSQKTHPLRKYNNMLNDYKERYKPEVRESI 2911
Db 2912 KALLAIGWSEHSEVDIPSNNSSMRQSKSGRPPEI--VTDATPPDYNNPVPVMTNL 2969
Qy 2909 KGLLAIGWSEHSEVDIPSNNSSMRQSKSGRPPEI--VTDATPPDYNNPVPVMTNL 2969
Db 2970 TLRSEWONABRLADNADIMAKCKEEL 2998
Qy 2964 TLRSEWONABRLADNADIMAKCKEEL 2998

RESULT 2

T99144

partial CDS - Caenorhabditis elegans

C1:Species: Caenorhabditis elegans

C1:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C1:Accession: T99144

R1:Palley, A.; Gactung, S.

Submitted to the EMBL data library, July 1996

A1:Description: The sequence of C. elegans cosmid K11C4.

A1:Reference number: 220577

A1:Accession: T99144

A1:Status: preliminary; translated from GB/EMBL/DBJ

A1:Molecular type: DNA

A1:Residue: 1-5107 <PAU>

A1:Experimental source: UNIPROT:Q94279; UNIPARC:UPI00011013D; EMBL:U64854; P1DN:AA18318.1;

A1:Gene: CEBP-unc-68

A1:Map position: 5

A1:Interons: 27/1; 64/3; 92/3; 127/1; 158/2; 1222/2; 1300/2; 1347/2; 1391/1; 1419/3; 1517/3; 3269/2; 3313/2; 3466/1; 3519/3; 3615/3; 3629/3; 3658/2; 3710/1; 3741/3; 3779/2; 3810/3

C1:Superfamily: Ryanodine receptor; transcritpion initiation factor sigma region 1 homolo

Query Match 43.4%; Score 6828; DB 2; Length 5107;
Beet Local Similarity 45.0%; Pred. No. 0;
Matches 1407; Conservative 519; Mismatches 850; Indels 350; Gaps 52;
Qy 113 MYLACIATSSSODKCLAFDVGLOHSGGACWMTLTPASRSGRGEKRYGDDLIIVSVAT 172
Db 1 MYLACIATSSSODKCLAFDVGLOHSGGACWMTLTPASRSGRGEKRYGDDLIIVSVAT 60
Qy 173 ERYLHTTK---ENEVSI-----VVASPHVTHMSVOPVGTGI 205
Db 61 ERYLHTTK---ENEVSI-----VVASPHVTHMSVOPVGTGI 205
Qy 206 SMKAYVGTVEGDDVLRFFHGDECLTIPSTWTKDGGQNTVYBGSVMSQASLWLELA 265
Db 121 MTRNMGFLRFNDVLRFFHGDECLTIPSTWTKDGGQNTVYBGSVMSQASLWLELA 180
Qy 266 RTKAGGFLNTPHRIHTTGRVYGVNDONELVYVSEBATTLSACACILAOEDODOK 325
Db 181 RTKAGGFLNTPHRIHTTGRVYGVNDONELVYVSEBATTLSACACILAOEDODOK 239
Qy 326 VLBDKDLVETGAPITVYGDSTVYVHSETGLMLSYKSYETKKGGVGVKEKQALIHBEK 385
Db 326 VLBDKDLVETGAPITVYGDSTVYVHSETGLMLSYKSYETKKGGVGVKEKQALIHBEK 385

Dp	1442	AGGTGTTCAACCGCTGATCTGAGGTGATCAAGGCGCATATGTGTGGGACAACAGAGACC	1501
Qy	2276	AAGTATTCAAACCCCTCACTGAAGTCATACAGGACCTTGACGAGATACAGCGGCTT	2335
Dp	1382	AGGAGATCATTAACCCCGCGGCAAGTCGAACTTCTTCAAGGCTATGGGTGCGCAATG	1441
Qy	2216	AGGAATGATCGAACCCTGCGCGGCAAGGCACTTCTTCAAGGCAATTGGAGTGGCTTCC	2275
Dp	1332	TGAGTTATCTGTGTGGCCCTGCAAGAGTCCATCATGGACTTTTACTGGGATCACTCTCA	1381
Qy	2156	TGCACTTACCTGTGGGCGCTGCAAGAGTCCATCATGGACTTCTTCACTGCACTACAGCA	2215
Dp	1262	AGAACTTACCTTGAGAGCGAGGAGGTATACAGACAGCGGTGAACCTCATCAACTGCAAG	1321
Qy	2086	AGAACTTACCTGCGAACTCAAGCCGGTAAACAGACACAGTGAACCTGGTCACTGCAACG	2155
Dp	1202	TTACTGTGGCGCTCTTTCGCTTTATTCGAACCTCACTGATAGGCAACCTGACTGGC	1261
Qy	2036	TCACTTGGCGCACTCTTCAAGGTTCAATTCAAGCTCACTGTGAGAGCACAACTTGACTGGC	2095
Dp	1142	AGGGTTTGGGTGTGGCGCTGACGAGTGGCGCGGAGAGAGAACATGCAATGACGAGT	1201
Qy	1976	AAGGTCTGGGCGTGGGTCTGGAAGGTGGCGCGGAGAGAGAACATGCAATGACGAGT	2035
Dp	1082	GGTTGATGAACCTCTGCAACAGTGTGAGACTTGAAGCGCTTGAGCGGCAACCAAGCGG	1141
Qy	1916	GCCTCATGAACCTCTGTCTCCGTCTCGATCTTGAAGCTTGAAGCTTGGAGAGAACCAAGGCTG	1975
Dp	962	TGATGACCAACCTCAAGCTGGGTATTCGATCTCAAGGGGTGGCAACCTGCACTGTCAAG	1021
Qy	1856	TGGGTATGTGAAACAATTGAAAGCAAGAAAGACGTGGGCTTCTTCACTGATCGCG	1915
Dp	1022	CGGCAATTTGAATTAACCTGAGAGAGAGAGAGAGAGCTTCTTCTTTCATTCGCGG	1081
Qy	1736	GGGTTGCGGAATGGTGTCTTCTGCACTCTCCGCGCTGCCAAAGGCTGCGCCAGAGATGG	1735
Dp	902	GGGTGGCAGAGATGGTGTGTTTTCATGATGGGAGCCCGCGGCAAGAGAGATGG	961
Qy	1796	TCATGAGACTTTTCAAGCTCGGTATTTAGTATCTGAGGGGCGGCAATTTGATATCAGA	1855
Dp	962	TGATGACCAACCTCAAGCTGGGTATTCGATCTCAAGGGGTGGCAACCTGCACTGTCAAG	1021
Qy	1676	ACGAAACAAGAAATGGAGAAACAAAGGCTCTTATTCACCAAGCGGGGTGGCGGACGCTG	1735
Dp	842	ATGAGCAAGAGTTTGAAGAGAGCAAGAGCTGTGTCTCACACAGGCAACGTCTTCAACGAG	901
Qy	1736	GGGTTGCGGAATGGTGTCTTCTGCACTCTCCGCGCTGCCAAAGGCTGCGCCAGAGATGG	1735
Dp	902	GGGTGGCAGAGATGGTGTGTTTTCATGATGGGAGCCCGCGGCAAGAGAGATGG	961
Qy	1616	GGAGGAAAGAGAGAGGGGTGGAGAGACAGAGGCTGAAGACGAGGCAAGCTCAAGTATAC	1675
Dp	786	----AGACGATGAGAGCGGCTGAGAGATGAGAGGCAAGAGATCCCAACCGGCTCTTA	841
Qy	1496	CCACTCTTCTGTGCGCGGTCCATGACTGAGAGGTCCGCGCTTTGACAGAGATCTCTAT	1555
Dp	668	CGACTTTTTCGCAATTAAGCGAGACGAGAGGCAACAGAGAGTCTTGGCCAGAGACCACTCT	727
Qy	1556	ACATGCTCTTACGCAACATCATATAGCGAAGTCCCTGTGAGAGAGAGAGAGAGAGGGGTG	1615
Dp	728	ATATGTTCTTACGCTGATGATCATGCGCAAGTCTTGTGTGAGAGAGAGAGAGAGAG--	785
Qy	1436	TGAAGAAAGTGAACGTGTGGAGAGAGGTGAGAGGCTGAGAGCTGACCCCTCAAGGCTGTCA	1495
Dp	608	CCAGAGAGAGAGAGGCTTGAAGAGAGCAAGGTAAACCGGACCAAGTTATCAACACTGGTAA	667
Qy	1496	CCACTCTTCTGTGCGCGGTCCATGACTGAGAGGTCCGCGCTTTGACAGAGATCTCTAT	1555
Dp	668	CGACTTTTTCGCAATTAAGCGAGACGAGAGGCAACAGAGAGTCTTGGCCAGAGACCACTCT	727
Qy	1556	ACATGCTCTTACGCAACATCATATAGCGAAGTCCCTGTGAGAGAGAGAGAGAGAGGGGTG	1615
Dp	728	ATATGTTCTTACGCTGATGATCATGCGCAAGTCTTGTGTGAGAGAGAGAGAGAGAG--	785
Qy	1616	GGAGGAAAGAGAGAGGGGTGGAGAGACAGAGGCTGAAGACGAGGCAAGCTCAAGTATAC	1675
Dp	786	----AGACGATGAGAGCGGCTGAGAGATGAGAGGCAAGAGATCCCAACCGGCTCTTA	841
Qy	1676	ACGAAACAAGAAATGGAGAAACAAAGGCTCTTATTCACCAAGCGGGGTGGCGGACGCTG	1735
Dp	842	ATGAGCAAGAGTTTGAAGAGAGCAAGAGCTGTGTCTCACACAGGCAACGTCTTCAACGAG	901
Qy	1736	GGGTTGCGGAATGGTGTCTTCTGCACTCTCCGCGCTGCCAAAGGCTGCGCCAGAGATGG	1735
Dp	902	GGGTGGCAGAGATGGTGTGTTTTCATGATGGGAGCCCGCGGCAAGAGAGATGG	961
Qy	1796	TCATGAGACTTTTCAAGCTCGGTATTTAGTATCTGAGGGGCGGCAATTTGATATCAGA	1855
Dp	962	TGATGACCAACCTCAAGCTGGGTATTCGATCTCAAGGGGTGGCAACCTGCACTGTCAAG	1021
Qy	1856	TGGGTATGTGAAACAATTGAAAGCAAGAAAGACGTGGGCTTCTTCACTGATCGCG	1915
Dp	1022	CGGCAATTTGAATTAACCTGAGAGAGAGAGAGAGAGCTTCTTCTTTCATTCGCGG	1081
Qy	1916	GCCTCATGAACCTCTGTCTCCGTCTCGATCTTGAAGCTTGAAGCTTGGAGAGAACCAAGGCTG	1975
Dp	1082	GGTTGATGAACCTCTGCAACAGTGTGAGACTTGAAGCGCTTGAGCGGCAACCAAGCGG	1141
Qy	1976	AAGGTCTGGGCGTGGGTCTGGAAGGTGGCGCGGAGAGAGAACATGCAATGACGAGT	2035
Dp	1142	AGGGTTTGGGTGTGGCGCTGACGAGTGGCGCGGAGAGAGAACATGCAATGACGAGT	1201
Qy	2036	TCACTTGGCGCACTCTTCAAGGTTCAATTCAAGCTCACTGTGAGAGCACAACTTGACTGGC	2095
Dp	1202	TTACTGTGGCGCTCTTTCGCTTTATTCGAACCTCACTGATAGGCAACCTGACTGGC	1261
Qy	2086	AGAACTTACCTGCGAACTCAAGCCGGTAAACAGACACAGTGAACCTGGTCACTGCAACG	2155
Dp	1262	AGAACTTACCTTGAGAGCGAGGAGGTATACAGACAGCGGTGAACCTCATCAACTGCAAG	1321
Qy	2156	TGCACTTACCTGTGGGCGCTGCAAGAGTCCATCATGGACTTCTTCACTGCACTACAGCA	2215
Dp	1332	TGAGTTATCTGTGTGGCCCTGCAAGAGTCCATCATGGACTTTTACTGGGATCACTCTCA	1381
Qy	2216	AGGAATGATCGAACCCTGCGCGGCAAGGCACTTCTTCAAGGCAATTGGAGTGGCTTCC	2275
Dp	1382	AGGAGATCATTAACCCCGCGGCAAGTCGAACTTCTTCAAGGCTATGGGTGCGCAATG	1441
Qy	2276	AAGTATTCAAACCCCTCACTGAAGTCATACAGGACCTTGACGAGATACAGCGGCTT	2335
Dp	1442	AGGTGTTCAACCGCTGATCTGAGGTGATCAAGGCGCATATGTGTGGGACAACAGAGACC	1501

QY	2336	TGGTCACTCCAGGTGGGAGCGCTGCGGTGTTCTGTTCTTAATCTCCCAATGC	2335
Db	1502	TGCGCCACTCCCGTCTGTGGAGCGCCGTCGGGGCTTCTCTTCTCTTCCCAATGC	1561
QY	2396	AGGACAACTGTGAGACCACTGTCGAGGTGACCTGTGAGAGAACTCTCCATCTGC	2455
Db	1562	AGGACAAAGCTCAATGAACTTCTCTCAGGTGCGCTCTCGAAGAACTCTCAACTGC	1621
QY	2456	AGAAAGCAATGATCCCAATGATGCTGTCATGCTTGAAGGAAATGTTTAATGTTCAA	2515
Db	1622	AGAAAGCAATGATCAATGATGCTCTCTATGCTGAGGGTAATGTGTGAACGGACCA	1681
QY	2516	TCGGCAAGCAATGATGAGCACTAGTAAGTAATGGCTCCCAAGTGAATCTGATCTGA	2575
Db	1682	TCGGCAAGCAAGATGATGAGCACTAGTGAAGACCGCTCCAAAGTGAAGTATCTGA	1741
QY	2576	AATATCTTGACATTTTCTCAAGTGAAGACCTGACCTCAAGGCCAGGTTCCAGGAGA	2635
Db	1742	GGTACTTGAAATGTTCTTAATGACTGGAGACTCAACAGTCCACACTTTCAGAGAT	1801
QY	2636	TATGATGCCAATTAACGACGGCTGGTGTGCTGCCAAGACTTCAAGAGAGAAATGGAACAAC	2695
Db	1802	TGGAATGAAACAAGAGACGAAACATTAATCAGCGAGGATTTAAGAAATAGATGAACGC	1861
QY	2696	AGAAAGCTTAATCTCCCGAAGAAATTCGAGTTCTCTTAGCTGTGAGAGACGAACACG	2755
Db	1862	AGAAATATTAACAACAAGAGAAATCAATCTCTGTGATGTGTGAATGTGAACACACG	1921
QY	2756	ACGGCAAGTAAAGACTAATCGGTTCTGCGACCGTTTCCACGAGCTGCCAAGAGATCG	2815
Db	1922	ACGGCAAGTAAATTAATGATGAAATTAATGAGCGCTTCCACAACTCAAGCAAGAGAGATCG	1981
QY	2816	GGTTTAATCTGGCGCTGTTACTGACTTAATCTGTGTGAACATATATGCCGACGAGCTTAGT	2875
Db	1982	GCTTCAACTGGCAGATGTGCTCAACCACTTGTCCGACCAATGCCCAACGACCAAGCTC	2041
QY	2876	TGGACAGCTTCTGAGAGACGGCAGAGTTCAAGTCTGAATCTTGAACCAATCTCTGGGCC	2935
Db	2042	TGCGTAGGTTCTTGAAGACACGGGTTCAAGTCTCAATTACTTGAAACATTTCTTGGGTC	2101
QY	2936	GTATCGAATCATGGGGGCTCAACAGCGCATCGAGCGTGTCTAATCTTGAGATCAAGAGT	2995
Db	2102	GTATGAAATCTTAGGCAAGCTTAACGATACGAACAGTGTACTTGAATTAAGAGAG	2161
QY	2996	CTAATA 3001	
Db	2162	AAACA 2167	

	RESULT 3			
	AF009344			
LOCUS	APF009344	866 bp	mRNA	linear INV 17-APR-2000
DEFINITION	Heliopsis virescens ryanodine receptor (<i>ryr</i>) mRNA, partial cds.			
ACCESSION	AF009344			
VERSION	AF009344.1	GI:4102114		
KEYWORDS	.			
SOURCE	. Heliopsis virescens (tobacco budworm)			
ORGANISM	Heliopsis virescens Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuidae; Noctuidae; Heliothinae; Heliothis. . 1 (bases 1 to 866) Puente,E., Sumer,M., Evans,A.D., McCafferty,A.R. and Windas,J.D. Identification of a polymorphic ryanodine receptor gene from <i>Heliopsis virescens</i> (Lepidoptera: noctuidae) Insect Biochem. Mol. Biol. 30 (4), 335-347 (2000)			
JOURNAL	PUBMED	10727900		
REFERENCES	2 (bases 1 to 866) Puente,E. and Windas,J.D. Direct Submission Submitted (18-JUN-1997) Biologie et Pathologie Digestive, INSERM U151, Institut Louis Bugnard. CHU Rangueil L3, Toulouse 31403 CEDEX			
AUTHORS	TITLE			
JOURNAL				

FEATURES
SOURCE

Location/Qualifiers
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ORIGIN

Query Match 27.8%; Score 835.6; DB 2; Length 866;
Best Local Similarity 97.8%; Pred. No. 2e-173;
Matches 847; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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1 CACTTGAAGAACAAGAAAGAGTGGCTTTTTCATGCTCGCGGCTCATGAATCC 60
1930 TGCCTCCGCTCGATCTTGAACGCTTGAAGAAACAAGGCTGAAGCTGCTGGCGTG 1989
61 TGCCTAGTGTCTGATCTTGAACGCTTGAAGAAACAAGGCTGAAGCTGCTGGCGTG 120
1990 GGTCTGAAGAGTGGCGGGAAGAAACAATGATACCGCGGCTCATGCTGGCACTC 2049
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301 CGGCTGCAAGAGTCAATGAGCTTCTAATGAGCACTCACTCAAGCAAGAACTGATGAC 360
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QY 2530 GTGACACATGATGAAATGGCGCTCCCAAGTGAACCTGATCTGAAATATCTTCACATG 2589
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QY 2650 GACGCTGGTGTGCTCCCAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2709
DB 781 GACGCTGGTGTGCTCCCAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 840
QY 2710 CCGAAGAAATGAGTTCCTCTAGC 2735
DB 841 CCGAAGAAATGAGTTCCTCTAGC 866

RESULT 4

OCRR

LOCUS OCRR 15361 bp mRNA linear MAR 10-MAR-2001
DEFINITION Rabbit skeletal muscle mRNA for ryanodine receptor.
ACCESSION X15750
VERSION X15750.1 GI:1709

KEYWORDS

calcium binding protein; channel protein; receptor; ryanodine receptor

SOURCE

ORGANISM

Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus

REFERENCE

AUTHORS

Takekoshi, H., Nishimura, S., Matsumoto, T., Ishida, H., Kangawa, K.,
Miyahara, N., Matsuo, H., Ueda, M., Hamaoka, M., Hirose, T. and Numa, S.
Primary structure and expression from complementary DNA of skeletal
muscle ryanodine receptor
Nature 339 (6224), 439-445 (1989)

JOURNAL

PUBMED

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FEATURES

SOURCE

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